DSP-12, 1656 Base Pairs

AAGCAGTGGTAACAACGCAGAGTACGCGGGCGAGGAGAATATCTTGCTGGGAGTGGACT TTTCCAGTAAGGAAAGTAAAAGCTGCACCATTGGGA**TG**GTTCTCCGACTGTGGAGCGAC CATATTTAAGCCTGTGTCTGTCCAGGCCATGTGGTCTGCCCTGCAGGTGCTTCACAAGG CCTGCGAAGTGGCCCGGAGGCACAACTACTTCCCCGGGGGTGTAGCTCTCATCTGGGCT ACCTACTATGAGAGCTGCATCAGCTCCGAGCAGAGCTGCATCAACGAGTGGAACGCCAT GCAGGACCTGGAGTCTACGCGGCCCGACTCCCCCGCGCTATTTGTGGACAAGCCCACTG AAGGGGAAAGGACCGAGCGCCTCATCAAAGCCAAGCTCCGAAGCATCATGATGAGCCAG GATCTAGAAAATGTGACTTCCAAAGAGATTCGTAATGAATTAGAGAAACAGATGAATTG TAACTTGAAGGAACTCAAGGAATTTATAGACAATGAGATGCTACTTATCTTGGGACAGA TGGACAAGCCCTCCCTTATCTTCGATCATCTTTATCTCGGCTCTGAATGGAATGCATCC AATCTGGAGGAACTGCAGGGCTCAGGGGTTGATTACATTTTAAATGTTACCAGAGAAAT CGATAATTTTTTCCTGGCTTATTTGCATATCATAACATCCGAGTCTACGATGAAGAGA CCACAGACCTCCTCGCCCACTGGAATGAAGCGTATCATTTTATAAACAAAGCGAAGAGG AACCATTCCAAGTGCCTGGTGCATTGCAAAATGGGCGTGAGTCGCTCGGCCTCCACAGT CATAGCCTATGCAATGAAGGAATTCGGCTGGCCTCTGGAAAAAGCATATAACTATGTAA AGCAGAAGCGCAGCATCACGCGCCCCAACGCGGGCTTTATGAGGCAGCTGTCTGAGTAT CAGCAGCCTCCAGCAGCCTGTGGATGACCCTGCAGGACCTGGCGACTTCTTGCCAGAGA CCCCAGATGGCACCCCGGAAAGCCAGCTGCCCTTCTTGGATGATGCCGCCCAGCCCGGC TTAGGGCCCCCCTCCCCTGCTGTTTCCGGCGACTCTCAGACCCCCTTCTGCCTTCCCC AGGAAGCTGCTCCACCTGCAGAGGTGCACAGGCCGGCCAGACAGCCCCAGCAAGGTTCC GGACTCTGTGAGAAGGATGTGAAGAAGAAACTAGAGTTTGGGAGTCCCAAAGGTCGGAG CGGCTCCTTGCTGCAGGTGGAGGAGGACGGAAAGGGAGGAGGGCCTGGGAGCAGGAGGT GGGGGCAGCTTCCAACCCAGCTCGATCAAAACCTGCTCAACTCGGAGAACCTAAACAAC AACAGCAAGAGGAGCTGTCCCAACGGCATGGAGGTAGGCAGAGCCCGGCCTGCAGGGTG GCACACCCCATCCCTTCCATCCCACTCTAATTGGCCTACCTCAGCCTCTGTAGTAGGGA AGCTCCCATCTCCAGGGACCTGAGGGTTCTTTCACAGGGTGATTCTGCTGGTGGGTACG TAGTGCATACCTTATATAGCAAATTGAGAATCTGTTGGGAATAACACATATCTCTGCAC ACCATCTTCACCCCATGTACCTTATTCATACCCTGGGCAGGGCTTCCAACTCAATTTCT AΑ

DSP-12, 552 Amino Acids

MVLRLWSDTKIHLDGDGGFSVSTAGRMHIFKPVSVQAMWSALQVLHKACEVARRHNYFP GGVALIWATYYESCISSEQSCINEWNAMQDLESTRPDSPALFVDKPTEGERTERLIKAK LRSIMMSQDLENVTSKEIRNELEKQMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLY LGSEWNASNLEELQGSGVDYILNVTREIDNFFPGLFAYHNIRVYDEETTDLLAHWNEAY HFINKAKRNHSKCLVHCKMGVSRSASTVIAYAMKEFGWPLEKAYNYVKQKRSITRPNAG FMRQLSEYEGILDASKQRHNKLWRQQTDSSLQQPVDDPAGPGDFLPETPDGTPESQLPF LDDAAQPGLGPPLPCCFRRLSDPLLPSPEDEAGSLVHLEDPEREALLEEAAPPAEVHRP ARQPQQGSGLCEKDVKKKLEFGSPKGRSGSLLQVEETEREEGLGAGRWGQLPTQLDQNL LNSENLNNNSKRSCPNGMEVGRARPAGWHTPSLPSHSNWPTSASVVGTTGTRHHTQLIF FYCLLWAPSSHLQGPEGSFTG

The second secon

DSP-13, 1527 Base Pairs

CCTGGGAAGAAGTTATCTATCTCTCGAGTGACATTCAAGATATACCGTACCCCTCGGTTCTGTA ${\tt AGTCCTCTAAGTTGGAGGCATTCCATTCTGAGCCGGCCCC} \textbf{ATG} \texttt{ACCCTGAGCACGTTGGCCCGC}$ AAGAGGAAGGCGCCCCTCGCTTGCACCTGCAGCCTCGGTGGCCCCGACATGATTCCTTACTTCT CCGCCAACGCGGTCATCTCGCAGAACGCCATCAACCAGCTCATCAGCGAGAGCTTTCTAACTGT CAAAGGTGCTGCCCTTTTTCTACCACGGGGAAATGGCTCATCCACACCAAGAATCAGCCACAGA CGGAACAAGCATGCAGGCGATCTCCAACAGCATCTCCAAGCAATGTTCATTTTACTCCGCCCAG AAGACAACATCAGGCTGGCTGTAAGACTGGAAAGTACTTACCAGAATCGAACACGCTATATGGT AGTGGTTTCAACTAATGGTAGACAAGACACTGAAGAAAGCATCGTCCTAGGAATGGATTTCTCC TCTAATGACAGTAGCACTTGTACCATGGGCTTAGTTTTGCCTCTCTGGAGCGACACGCTAATTC ATTTGGATGGTGATGGTGGTTCAGTGTATCGACGGATAACAGAGTTCACATATTCAAACCTGT ATCTGTGCAGGCAATGTGGTCTGCACTACAGAGCTTACACAAGGCTTGTGAAGTCGCCAGAGCG CATAACTACTACCCAGGCAGCCTATTTCTCACTTGGGTGAGTTATTATGAGAGCCATATCAACT CAGATCAATCCTCAGTCAATGAATGGAATGCAATGCAAGATGTACAGTCCCACCGGCCCGACTC TTAAGGGAGATCATGATGCAGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGT TGGAAATGCAAATGGTGTGCAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGT GATCCTTGGTCAAATGGATAGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGG AATGCCTCCAACTTAGAGGACTTACAGAACCGAGGGGTACGGTATATCTTGAATGTCACTCGAG AGATAGATAACTTCTTCCCAGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGC AACGGATCTCCTGGCGTACTGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGA TCTAAATGCCTTGTGCACTGCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATG CAATGAAGGAATATGGCTGGAATCTGGACCGAGCCTATGACTATGTGAAAGAAGAAGACGAACGGT AACCAAGCCCAACCCAAGCTTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGC TTCCTAGGCTTGATTCATGGAGGGAGGGACAAGCCCTGGGGAGAAAAGCACAGAATTTGAGT CAGTAGATCTGGTTTCCATTCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACAT TTCTCATCCTTACCTGACCCCATCTATAAAATGAAAATCAAGAGATCCATCTCACAGGGTTATT

DSP-13, 509 Amino Acids

MTLSTLARKRKAPLACTCSLGGPDMIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGS STPRISHRRNKHAGDLQQHLQAMFILLRPEDNIRLAVRLESTYQNRTRYMVVVSTNGRQDTEES IVLGMDFSSNDSSTCTMGLVLPLWSDTLIHLDGDGGFSVSTDNRVHIFKPVSVQAMWSALQSLH KACEVARAHNYYPGSLFLTWVSYYESHINSDQSSVNEWNAMQDVQSHRPDSPALFTDIPTERER TERLIKTKLREIMMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFE HVFLGSEWNASNLEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKFISKAKKHGSKCLVHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEE YQGILLASFLGLIHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

A DSP13 Alternate Splice Variant, 723 Base Pairs

CTGCCCGGCTTCTAACAGGCCACTGACCGGTACTCACTGGGGACCCACGCTCTAAGTTGTTGAT CTCTAGAACCGATTTTGGAAAAGGATTTGCCTTATTGAAGAAGACAGGATCATTCTTCTT AGACCTACTGAACGTGAACGAACAGAAAGGCTAATTAAAACCAAATTAAGGGAGATC**ATG**ATGC AGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGTTGGAAATGCAAATGGTGTG CAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGTGATCCTTGGTCAAATGGAT AGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGGAATGCCTCCAACTTAGAGG AGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGCAACGGATCTCCTGGCGTAC TGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGATCTAAATGCCTTGTGCACT GCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATGCAATGAAGGAATATGGCTG GAATCTGGACCGAGCCTATGACTATGTGAAAGAAGACGAACGGTAACCAAGCCCAACCCAAGC TTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGCTTCCTAGGCTTGATTCATG GAGGGAGGGACAAGCCCTGGGGAGAAAAGCACAGAATTTGAGTCAGTAGATCTGGTTTCCAT TCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACATTTCTCATCCTTACCTGACC CCATCTATAAAA**TGA**AAATCAAGAGATCCATCTCACAGGGTTATTGTGAATAAAAATGTGTTTG AATGTTTATAAAAAAAAAAAAAAAAAAAAA

B DSP13 Alternate Splice Variant, 241 Amino Acids

MMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFEHVFLGSEWNASN LEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKFISKAKKHGSKCL VHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEEYQGILLASFLGL IHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

100	NLSQF NLSQF KLLPH EISBH DISSH DISSH DISSH DLLAH NLSRY LS		
90	SOLDRO-PNSATDSDGSPLSNSQPSFPVEILPFLYLGCRKDSTNLDVLEFFGIKYILNVTPNLPMLFENRGEFKYKQIPISDHHSQNLSQF DRELPSSATESDGSPVSQPRFPVQILPFLYLGCRKDSTNLDVLEFFGIKYILNVTPNLPMFFEHGGFFFYKQIPISDHHSQNLSQF GLCEGKPROLLPHSCLSQPCLPVPSVGLTRILPHLYLGSGKDVLNKDLHTQNGISYVLNRSNSCPWFFEHGGFFFYKQIPISDHHSQNLSGF GLCEGKPROLLPHSCLSQPCLPVPSVGLTRILPHLYLGSGKDVLNKDLHTQNGISYVLNRSNSCPWFFE-GLFHYKQIPISDHYCEKLLPH PRQRIPPRGRENSNSDPRVPIYDGGPVEILPFLYLGSGYHRSKDHLDRLGITRLNVSRSCPWFFEGHYQYKCIPVEDNUKRDISSH PVPPSATEPLDLGCSSCGTPLHDQGGPVEILPFLYLGSRYHRRRDMLDRLGITRLNVSR		
80	PNL FENRGEFKY PNRFEHGGEFYY PNRFEHGGEFYY PNRFE-GLFHY PNRFE-GHYQY PNRFE-GHYQY IONFFP-GLFRY IONFFP-GLFRY IONFFP-GLFRY IONFFP-GLFRY IONFFP-GLFRY IONFFP-GLFRY IONFFP-GLFRY	18#82	ERTLGLSS ERTLGLSS ERSLRLE ETQVLCH ESQVLRPH ESQVLRTP ESETLPSTP EGILDRSKQ QGTLLRSFL
		170	NFMGQLLDFI NFMGQLLDFI NFMGQLLDFI NFLGQLLQFI SFMGQLLQFI SFMGQLLQFI SFMGQLLQFI GFMGQLEFY GFMRQLEFY GFMRQLEFY GFMRQLEFY GFMRQLEFY
99	GIKYILNYTP GIKYILNYTP GIRYILNYTP GITRYLNYSP GITRLNYSP GITRLNYSP HITRLNYSP GVOYILNYTR GENYTLNYTR GENYTLNYTR GENYTLNYTR	160	ANDRYDTVKMKSNISPNFNFMGQLLD LINDRYDFVKRKSNISPNFNFMGQLLD SDDRYRFVKDRRPSISPNFNFLGQLLE LIDERFEFVKQRRSTSPNFSFMGQLLQ LLEERFEFVKQRRSTISPNFSFMGQLLQ LLKERFDYIKQRRSTISPNFSFMGQLLQ LLKRRYNYVKQKRSTIRPNRGFMGQLLQ LDRRYDYVKRKSTIRPNAGFNRQLSE WKSALSIVRQNR-IGPNDGFLRQLCQ ANDRYDYKERTVTKPNPSFNRQLEE
20	TNLOVLEFFGT TNLOVLEFFGT ANLESLAKLGT LNKDLATQNGJ SDLQGLQACGG SRKDMLDALGG SRKCFLANLHJ SNLEELQGSGA GOTPKLQKLGG	150	MADAYDIVK LINDAYDIVK SIDDAYBIVK SIDDAYBIVK ALEENFEFVK KLEENFEFVK KLEENFEFVK ALEKNYNYK MIDRAYDYK MIDRAYDYK ALDRAYDYK ALDRAYDYK ALDRAYDYK ALDRAYDYK
	SFPVEIL PFLYLGCRKDSTNLDVLEFFGIKYIL NVTP—— SFPVQIL PYLYLGCRKDSTNLDVLEFFGIKYIL NVTP—— SFPVQIL PYLYLGSRRDSNLESLRKLGIRYIL NVTP—— VGLTRIL PYLYLGSRRDSNLESLRKLGIRYIL NVTP—— VGLTRIL PYLYLGSRVHRSSDLQGLQRCGITRVLNVSR—— GGPVEIL PFLYLGSRYHRRRDMLDRLGITRLINVSR—— GGPVEIL PFLYLGSRYHRRRDMLDRLGITRLINVSR—— GGPVEIL PFLYLGSRYHRSKCFFLRNLHITRLLNVSR—— GGPVEIL PFLYLGSRYHRSKCFFLRNLHITRLLNVSR—— GGPVEIL PFLYLGSRYHRSKCFFLRNLHITRLLNVSR—— GGPVEIL PFLYLGSRYHRSKCFFLRNLHITRLLNVSR—— GGPVEIL PHYLGSELNNSNLEELQGSGVDYIL NVTR—— ODFYTQIFEHVFLGSELNNSNLEDLQNRGVRYIL NVTR—— OPPCNEVTPRIYVGNASVRQDIPKLQKLGITHVLNRREGRS P eilp lylgsa an \$ g! y LNv	140 150 160 170 1808	ISRSYTVTVAYLHÖKLNLSKNORYDIVKHKKSNISPNFNFHGOLLDFERTLGLSS ISRSYTVTVAYLHÖKLNLSLNORYDEVKRKKSNISPNFNFHGOLLDFERTLGLSS VSRSYTVTVAYLHÖKNISLNORYDEVKRKKSNISPNFNFHGOLLDFERTLGLSS VSRSYTVTVAYLHÖKNISLNORYDEVKRKKSNISPNFNFHGOLLDFERSLRLE ISRSATICLAYLHÖKNRLDERFDFVKORRSISPNFSFHGOLLQLETQVLCH ISRSATICLAYLHKRAYLLERFEFVKORRSISPNFSFHGOLLQFESQVLAPP ISRSATICLAYLHKRKAYLERFEFVKORRSISPNFSFHGOLLQFESQVLAPS VSRSASTVIAYAHKRYCHLEKAYNYKOKRSITRPNAGFHROLSEYEGILDASKQ VSRSASTVIAYAHKRYKHOVRLERAYNYKOKRSITRPNAGFHROLSEYEGILDASKQ VSRSASTVIAYAHKRAYLHKRAYLKATVIKANYKKRSITRPNAGFHROLSEYEGILDASKQ VSRSASTVIAYAHKRAYLHKRAYLHKAYLAYAYVKOKRSITRPNAGFHROLSEYEGILDASKG VSRSASTVIAYAHKRAYLHKRAYLAYAVAYAKRRIVIKPNPSFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLHKRAYLYAYLAYAVAKRRIVIKPNPSFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLHKRAYLAYAVAYAKRRIVIKPNPSFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLANFKG VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLANFKG VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLANFKG VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYAGILDAKA INTAKKA INTA
99	SOLORD-PHSATOSOGSPLSNSQPSFPVEILPFLYLGCRKDSTNLOVLEEFGIKYILNVTP DRELPSSATESOGSPVPSSQPRFPVQILPYLYLGCRKDSTNLOVLEEFGIKYILNVTP GATPPPVGLRASFPVQILPNLYLGSRRDSANLESLAKLGIRYILNVTP GLCEGKPAALLPHSLSQPCLPVPSVGLTRILPHLYLGSQKDVLNKOLMTQNGISYVLNASN PAQALPPAGAENSNSDPRVPTYDQGGPVEILPFLYLGSRYHASRKDMLDALGITALLNVSA PVPPSATEPLOLGCSSCGTPLHDQGGPVEILPFLYLGSAYHASRKDMLDALGITALLNVSA SERALISQCGKPVNVSYRPAYDQGGPVEILPFLYLGSAYHASKCFFLANLHITALLNVSS GANCOLKELKEFIDNEMLILGQADSPTQIFFHYLGSAYHASKCFFLANLHITALLNVSR QANCOLREFKEFIDNEMLYILGQADSPTQIFFHYLGSEWNASNLEDLQNRGVRYILNVTR GANCOLREFKEFIDNEMILYLGQADSPTQIFFHYLGSEWNASNLEDLQNRGVRYILNVTR	130	FPERISFIDER-RGKNCGVLYHCLRGISRSYTYTYRYLHQKLNLSKNDRYDTVKHKKSNISPNFNFNGQLLDFERTLGLSS FPERISFIDER-RSKKCGVLYHCLRGISRSYTYTYRYLHQKLNLSLNDRYDFVKRKKSNISPNFNFNGQLLDFERTLGLSS FPERISFIDER-LSQUCGVLYHCLRGISRSYTYTYRYLHQKLNLSLNDRYDFVKRKKSNISPNFNFNGQLLDFERTLGLSS FPERISFIDER-LSGQVLYHCLRGISRSRTIRITRIANTHKHRSSDDRYRFVKDRRFSISPNFNFLGGLLEYERTLKLR FRENISFIDSY-KNSGGRVLYHCQRGISRSRTICLRYLHRKKVRLDERFDFVKQRRGVISPNFSFNGQLLQLETQVLCH FNERIDFIDSI-KNRGGRVLYHCQRGISRSRTICLRYLHRKKWRLEERFFFVKQRRSIISPNFSFNGQLLQFESQVLRTF FQERIDFIDCY-REKGGRVLYHCGRGISRSPTICHRYLHKKKVRLEERFFFVKQRRSIISPNFSFNGQLLQFESQVLRTS HNERYHFINKR-KRNHSKLYHCKHGVSRSRSTVIRYRMKFFGHPLEKRYNYVKQKRSIIRPNRGFNRQLSEYEGILDRSKQ HNDTYKFISKR-KHGSKLYHCKHGVSRSRSTVIRYRMKFFGHNUDRRYVKQKRSIIRPNRGFNRQLSEYEGILDRSF FRANDFIDGALQKNGRVLYHCREGYSRSPTLVIRYLHRRQKNOVKSRLSTVRQNRE-IGPNDGFLRQLCQLNDRLRKG F eai FI# a k v1YHC aGISRSAL IRYIH 1 Ay ! kqrr ispNf F\$gQLL## 1
50	SOGSPLSNSOP GATPPPVGLRR GATPPPVGLRR ASLSQPCLPVPS SNSDPRVPTYDQ GCSCCTPLHDQ VVNVSYRPRYDQ TONEMLLILGQH LSDGSGCYSLPS	120	KNCGVL VHCLAG KKCGVL VHCLAG SCGVL VHCLAG SCGVL VHCQAG GCGRVF VHCQAG CRGRVL VHCQAG KGGRVL VHCQAG KGGRVL VHCQAG KGGRVL VHCQAG NISKCL VHCKAG VIVHC AG
10	SOLORO-PNSATOSOGSPLSNSQP DRELPSSATESOGSPLSNSQP GATPPYGLRA GLCEGKPAALLPMSLSQPCLPVPS PADALPPAGAENSNSDPRVPIYDQ PLSTSVPDSAESGCSSCGTPLYDQ PVPPSATEPLOLGCSSCGTPLHOQ SERALISQCGKPVNVSYRPAYDQ QMNCNLKELKEFIDNENLLILGQH QMVCNLREFKEFIDNENLLILGQH	110 110	FPERISFIDER-RGKNCGVLVHCLNG FPERISFIDER-LSGNCGVLVHCLNG FPERIFFIDER-LSGNCGVLVHCLNG LDKSIEFIDKR-KLSSCQVIVHCLNG FQERISFIDSV-KNGGGRVFVHCQNG FNERIDFIDSV-REKGGKVLVHCQNG FNERIDFIDCV-REKGGKVLVHCCNG HNERYHFINKR-KRNISKCLVHCKNG FRANDFIDGALAQKNGRVLVHCKNG FERANDFIDGALAQKNGRVLVHCKG
₩-		101	
	PYST1 MKP-7 MKP-4, hVH5 PRC1 MKP-2, MKP-5, MKP-5, MKP-12 OSP-12 OSP-12		PYST1 MKP-7, MVH5 PRC1 MKP-2, MKP-2, MKP-2, MKP-2, MKP-12 DSP-12 DSP-13

Figure 6

Alignment of DSP-12 and DSP-13

110
100
96
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70
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OSP-13 MTLSTLARKRKAPLACTCSLGGPOMIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGSSTPRISHRRNKHAGOLQQHLQAAFILLRPEONIRLAVRLESTYQNR

220 1 YESCI YESHI
111 120 130 140 150 160 170 180 190 200 210 220 10 10 10 10 10 10 10 10 10 10 10 10 10
200 RCEVARRHNYF RCEVARAHNYY
190 HSALQVLHKI
180 IIFKPVSVQARIIFKPVSVQAR
170 FSVSTNGRHI FSVSTDNRVF
160 TKTHLUGDGG
150 HYLRLHSD HGLYLPLHSD
140 + FSSNDSSTCT
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0SP-12 0SP-13

330 LGSEHNA LGSEHNA
320 PSLIFOHLY PTQIFEHVF
310 HLILGONDK HIVILGONDS
300 KELKEFIDNE
290 LEKOMNCNL)
280 NVTSKEIRNE NITSKEIRTE
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			DSP-12

